

IUBMB Enzyme Nomenclature

EC 3.3.2.6

Common name: leukotriene-A₄ hydrolase

Reaction: (7*E*,9*E*,11*Z*,14*Z*)-(5*S*,6*S*)-5,6-epoxyicosa-7,9,11,14-tetraenoate + H₂O = (6*Z*,8*E*,10*E*,14*Z*)-(5*S*,12*R*)-5,12-dihydroxyicosa-6,8,10,14-tetraenoate

Other name(s): LTA₄ hydrolase; LTA4H

Systematic name: (7*E*,9*E*,11*Z*,14*Z*)-(5*S*,6*S*)-5,6-epoxyicosa-7,9,11,14-tetraenoate hydrolase

Comments: Converts 4,5-leukotriene A₄ into leukotriene B₄. Highly specific. Not identical with [EC 3.3.2.3](#) epoxide hydrolase.

Links to other databases: [BRENDA](#), [EXPASY](#), [KEGG](#), [ERGO](#), [PDB](#), CAS registry number: 90119-07-6

References:

1. Evans, J.F., Dupuis, P. and Ford-Hutchinson, A.W. Purification and characterisation of leukotriene A₄ hydrolase from rat neutrophils. *Biochim. Biophys. Acta* 840 (1985) 43-50. [Medline UI: [85200023](#)]
2. Minami, M., Ohno, S., Kawasaki, H., Rådmark, O., Samuelsson, B., Jörnvall, H., Shimizu, T., Seyama, Y. and Suzuki, K. Molecular cloning of a cDNA coding for human leukotriene A₄ hydrolase - complete primary structure of an enzyme involved in eicosanoid synthesis. *J. Biol. Chem.* 262 (1987) 13873-13876.

[EC 3.3.2.6 created 1989]

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[Return to EC 3.3 home page](#)

[Return to EC 3 home page](#)

[Return to Enzymes home page](#)

[Return to IUBMB Biochemical Nomenclature home page](#)

Home Search Results Queries

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1HS6

 Chains
E Value

Characteristics

Classification

Compound

Authors

Alignment stats

Alignment

STRUCTURE OF LEUKOTRIENE A4 HYDROLASE COMPLEXED WITH BESTATIN.

A

0.0

Deposited: 24-Dec-2000 Exp. Method: X Ray Diffraction

Resolution: 1.95 Å

Hydrolase

Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase

Thunnissen, M.M., Nordlund, P., Haeggstrom, J.Z.

Length: 610 Score: 1222.99bits (3163) E-value: 0.0 Identities: 610/610 (100%) Positives: 610/61 (100%) Gaps: 0/610 (0%)

| | | | | | | | |
|-------|------|------|-----|-----|------|------|------|
| | 1 | 10 | 20 | 30 | 40 | 50 | 60 |
| Query | PEIV | DTCS | LAS | PAS | VCRT | KHLH | LRCS |
| | 2 | 10 | 20 | 30 | 40 | 50 | 60 |
| Sbjct | PEIV | DTCS | LAS | PAS | VCRT | KHLH | LRCS |

1H19

 Chains
E Value

Characteristics

Classification

Compound

Authors

Alignment stats

Alignment

STRUCTURE OF [E271Q] LEUKOTRIENE A4 HYDROLASE

A

0.0

Deposited: 04-Jul-2002 Exp. Method: X Ray Diffraction

Resolution: 2.10 Å

Hydrolase

Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: YES

Rudberg, P.C., Tholander, F., Thunnissen, M.M., Haeggstrom, J.Z.

Length: 610 Score: 1221.84bits (3160) E-value: 0.0 Identities: 609/610 (100%) Positives: 610/61 (100%) Gaps: 0/610 (0%)

| | | | | | | | |
|-------|------|------|-----|-----|------|------|------|
| | 1 | 10 | 20 | 30 | 40 | 50 | 60 |
| Query | PEIV | DTCS | LAS | PAS | VCRT | KHLH | LRCS |
| | 2 | 10 | 20 | 30 | 40 | 50 | 60 |
| Sbjct | PEIV | DTCS | LAS | PAS | VCRT | KHLH | LRCS |

1GW6

 Chains
E Value

Characteristics

Classification

Compound

Authors

Alignment stats

Alignment

STRUCTURE OF LEUKOTRIENE A4 HYDROLASE D375N MUTANT

A

0.0

Deposited: 07-Mar-2002 Exp. Method: X Ray Diffraction

Resolution: 2.20 Å

Hydrolase

Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: YES

Rudberg, P., Tholander, F., Thunnissen, M., Samuelsson, B., Haeggstrom, J.

Length: 610 Score: 1221.07bits (3158) E-value: 0.0 Identities: 609/610 (100%) Positives: 610/61 (100%) Gaps: 0/610 (0%)

| | | | | | | | |
|-------|------|------|-----|-----|------|------|------|
| | 1 | 10 | 20 | 30 | 40 | 50 | 60 |
| Query | PEIV | DTCS | LAS | PAS | VCRT | KHLH | LRCS |
| | 2 | 10 | 20 | 30 | 40 | 50 | 60 |
| Sbjct | PEIV | DTCS | LAS | PAS | VCRT | KHLH | LRCS |

1SQM

 Chains
E Value

Characteristics

Classification

Compound

Authors

Alignment stats

Alignment

STRUCTURE OF [R563A] LEUKOTRIENE A4 HYDROLASE

A

0.0

Deposited: 19-Mar-2004 Exp. Method: X Ray Diffraction

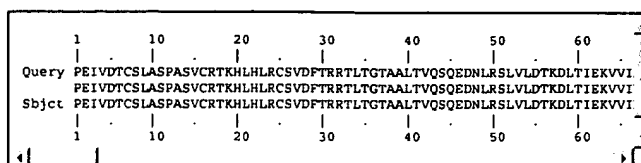
Resolution: 2.30 Å

Hydrolase

Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: R563A

Rudberg, P.C., Tholander, F.O.T., Andberg, M., Thunnissen, M.M.G.M.

Length: 610 Score: 1220.68bits (3157) E-value: 0.0 Identities: 609/610 (100%) Positives: 609/61 (100%) Gaps: 0/610 (0%)



1Z1W



Crystal structures of the tricorn interacting factor F3 from *Thermoplasma acidophilum*, a zinc aminopeptidase in three different conformations

Chains

A

E Value

4.07144E-20

Characteristics

Deposited: 07-Mar-2005 Exp. Method: X Ray Diffraction

Classification

Resolution: 2.70 Å

Compound

Hydrolase

Mol. Id: 1

Molecule: Tricorn Protease Interacting Factor F3

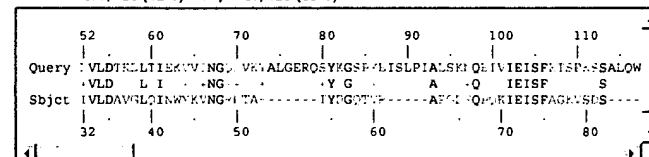
Authors

Kyrieleis, O.J.P., Goettig, P., Kiefersauer, R., Huber, R., Brandstetter, H.

Alignment stats

Length: 426 Score: 95.9005bits (237) E-value: 4.07144E-20 Identities: 108/426 (25%)
Positives: 177/426 (42%) Gaps: 57/426 (13%)

Alignment



1Z5H



Crystal structures of the Tricorn interacting Factor F3 from *Thermoplasma acidophilum*

Chains

A,B

E Value

4.07144E-20

Characteristics

Deposited: 18-Mar-2005 Exp. Method: X Ray Diffraction

Classification

Resolution: 2.30 Å

Compound

Hydrolase

Mol. Id: 1

Molecule: Tricorn Protease Interacting Factor F3

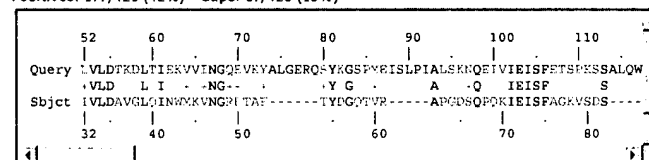
Authors

Kyrieleis, O.J.P., Goettig, P., Kiefersauer, R., Huber, R., Brandstetter, H.

Alignment stats

Length: 426 Score: 95.9005bits (237) E-value: 4.07144E-20 Identities: 108/426 (25%)
Positives: 177/426 (42%) Gaps: 57/426 (13%)

Alignment



2GTQ



Crystal structure of aminopeptidase N from human pathogen *N. meningitidis*

Chains

A

E Value

1.35851E-7

Characteristics

Deposited: 28-Apr-2006 Exp. Method: X Ray Diffraction

Classification

Resolution: 2.05 Å

Compound

Hydrolase

Mol. Id: 1

Molecule: Aminopeptidase N

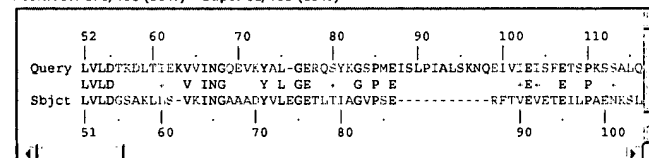
Authors

Nocek, B., Muligan, R., Bargassa, M., Joachimiak, A.

Alignment stats

Length: 481 Score: 54.299bits (129) E-value: 1.35851E-7 Identities: 111/481 (23%)
Positives: 170/481 (35%) Gaps: 61/481 (13%)

Alignment



1NNJ



Crystal structure Complex between the *Lactococcus lactis* Fpg and an abasic site containing DNA

Chains

A

E Value

2.10075

Characteristics

Deposited: 14-Jan-2003 Exp. Method: X Ray Diffraction

Classification

Resolution: 1.90 Å

Compound

Hydrolase

Mol. Id: 3

Molecule: Formamidopyrimidine DNA Glycosylase Mutation: P1G

Authors

Serre, L., Pereira de Jesus, K., Boiteux, S., Zelwer, C., Castaing, B.

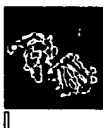
Alignment stats

Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

Alignment

| | | | | | | | |
|-------|---|-----|-----|-----|-----|-----|-----|
| | 281 | 290 | 300 | 310 | 320 | 330 | 3 |
| Query | TL AGDKSLNVAHEISHSWTGNVTNKIWHFWLNEGHTVY-----LEHICGRLFGEFFRH | | | | | | |
| | TL AG L N+ E+ W K + H + L+ I +L G R + | | | | | | |
| Sbjct | TLVAG---LGNIVYDEVL--WLAKIHPEKETNOLIESSIHLLHDSITIELKAI--RLGGSSIRTY | | | | | | |
| | 164 | 170 | 180 | 190 | 200 | 210 | 220 |

1PJI



Chains

Crystal structure of wild type *Lactococcus lactis* FPG complexed to a 1,3 propanediol containing DNA

E Value

2.10075

Characteristics

Deposited: 03-Jun-2003 Exp. Method: X Ray Diffraction

Classification

Resolution: 1.90 Å

Compound

Hydrolase/dna

Authors

Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase

Pereira, K., Serre, L., Zelwer, C., Castaing, B.

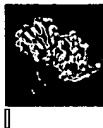
Alignment stats

Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

Alignment

| | | | | | | | |
|-------|---|-----|-----|-----|-----|-----|-----|
| | 281 | 290 | 300 | 310 | 320 | 330 | 3 |
| Query | TL AGDKSLNVAHEISHSWTGNVTNKIWHFWLNEGHTVY-----LEHICGRLFGEFFRH | | | | | | |
| | TL AG L N+ E+ W K + H + L+ I +L G R + | | | | | | |
| Sbjct | TLVAG---LGNIVYDEVL--WLAKIHPEKETNOLIESSIHLLHDSITIELKAI--RLGGSSIRTY | | | | | | |
| | 164 | 170 | 180 | 190 | 200 | 210 | 220 |

1PJJ



Chains

Complex between the *Lactococcus lactis* Fpg and an abasic site containing DNA.

E Value

2.10075

Characteristics

Deposited: 03-Jun-2003 Exp. Method: X Ray Diffraction

Classification

Resolution: 1.90 Å

Compound

Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase Mutation: P1G

Authors

Serre, L., Pereira de Jesus, K., Boiteux, S., Zelwer, C., Castaing, B.

Alignment stats

Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

Alignment

| | | | | | | | |
|-------|---|-----|-----|-----|-----|-----|-----|
| | 281 | 290 | 300 | 310 | 320 | 330 | 3 |
| Query | TL AGDKSLNVAHEISHSWTGNVTNKIWHFWLNEGHTVY-----LEHICGRLFGEFFRH | | | | | | |
| | TL AG L N+ E+ W K + H + L+ I +L G R + | | | | | | |
| Sbjct | TLVAG---LGNIVYDEVL--WLAKIHPEKETNOLIESSIHLLHDSITIELKAI--RLGGSSIRTY | | | | | | |
| | 164 | 170 | 180 | 190 | 200 | 210 | 220 |

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:50:03 ; Search time 189 Seconds
(without alignments)
1418.101 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|------------|--------------------|
| 1 | 3225 | 100.0 | 611 | 3 AAB08840 | Aab08840 Amino aci |
| 2 | 3225 | 100.0 | 611 | 8 ABM81460 | Abm81460 Tumour-as |
| 3 | 3225 | 100.0 | 611 | 9 ADW07254 | Adw07254 Human hep |
| 4 | 3225 | 100.0 | 611 | 9 ADZ04287 | Adz04287 Human leu |
| 5 | 3222 | 99.9 | 611 | 7 ADE25724 | Ade25724 Human pro |
| 6 | 3042.5 | 94.3 | 610 | 8 ADT66633 | Adt66633 Rat leuko |
| 7 | 2963 | 91.9 | 625 | 3 AAB58111 | Aab58111 Lung canc |
| 8 | 2696 | 83.6 | 532 | 8 ADL99491 | Adl99491 Human leu |

| | | | | | | | |
|----|--------|------|-----|---|----------|----------|-----------|
| 9 | 2438.5 | 75.6 | 480 | 8 | ADL99494 | Adl99494 | Human leu |
| 10 | 1464 | 45.4 | 587 | 8 | ADN23312 | Adn23312 | Bacterial |
| 11 | 1376.5 | 42.7 | 809 | 8 | ADN23545 | Adn23545 | Bacterial |
| 12 | 1338 | 41.5 | 613 | 4 | ABB71965 | Abb71965 | Drosophil |
| 13 | 1206.5 | 37.4 | 612 | 8 | ADS44280 | Ads44280 | Bacterial |
| 14 | 1134.5 | 35.2 | 671 | 6 | ABR52866 | Abr52866 | Protein s |
| 15 | 1134.5 | 35.2 | 671 | 7 | ADK62338 | Adk62338 | Disease t |
| 16 | 1134.5 | 35.2 | 671 | 8 | ADN19334 | Adn19334 | Bacterial |
| 17 | 1079 | 33.5 | 694 | 8 | ADN21345 | Adn21345 | Bacterial |
| 18 | 1059.5 | 32.9 | 623 | 2 | AAW02284 | Aaw02284 | Candida a |
| 19 | 1030.5 | 32.0 | 573 | 8 | ADS30208 | Ads30208 | Bacterial |
| 20 | 1018.5 | 31.6 | 584 | 9 | ABM96671 | Abm96671 | M. xanthu |
| 21 | 1006.5 | 31.2 | 650 | 5 | AAU72906 | Aau72906 | Human met |
| 22 | 1006.5 | 31.2 | 650 | 5 | ADR43717 | Adr43717 | Human pro |
| 23 | 1006.5 | 31.2 | 650 | 6 | ABP59205 | Abp59205 | Human ami |
| 24 | 1006.5 | 31.2 | 650 | 7 | ADD45336 | Add45336 | Human Pro |
| 25 | 1006.5 | 31.2 | 650 | 8 | ABM80228 | Abm80228 | Tumour-as |
| 26 | 1006.5 | 31.2 | 658 | 7 | ADC31289 | Adc31289 | Human nov |
| 27 | 1005.5 | 31.2 | 650 | 4 | AAB84214 | Aab84214 | Amino aci |
| 28 | 1001.5 | 31.1 | 650 | 7 | ADD45334 | Add45334 | Rat Prote |
| 29 | 1000 | 31.0 | 657 | 8 | ADR97314 | Adr97314 | Human RNP |
| 30 | 987 | 30.6 | 626 | 7 | ADM05614 | Adm05614 | Human pro |
| 31 | 954 | 29.6 | 569 | 8 | ADN26507 | Adn26507 | Bacterial |
| 32 | 947 | 29.4 | 671 | 8 | ADS28564 | Ads28564 | Bacterial |
| 33 | 929.5 | 28.8 | 588 | 8 | ADS27297 | Ads27297 | Bacterial |
| 34 | 929.5 | 28.8 | 588 | 8 | ADS26935 | Ads26935 | Bacterial |
| 35 | 929.5 | 28.8 | 641 | 8 | ADS26559 | Ads26559 | Bacterial |
| 36 | 887.5 | 27.5 | 650 | 8 | ADY05243 | Ady05243 | Plant ful |
| 37 | 880 | 27.3 | 540 | 8 | ADN26764 | Adn26764 | Bacterial |
| 38 | 874 | 27.1 | 581 | 8 | ADS28769 | Ads28769 | Bacterial |
| 39 | 800.5 | 24.8 | 724 | 5 | AAU72907 | Aau72907 | Human met |
| 40 | 800 | 24.8 | 725 | 5 | ABB77908 | Abb77908 | Amino aci |
| 41 | 800 | 24.8 | 725 | 8 | ADL14157 | Adl14157 | Novel hum |
| 42 | 766.5 | 23.8 | 416 | 4 | AAM25679 | Aam25679 | Human pro |
| 43 | 721 | 22.4 | 541 | 5 | ADR41508 | Adr41508 | Human CD- |
| 44 | 715.5 | 22.2 | 756 | 8 | ADJ67633 | Adj67633 | Human ova |
| 45 | 671.5 | 20.8 | 501 | 8 | ADJ71950 | Adj71950 | Human PMM |

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:03:01 ; Search time 47 Seconds
(without alignments)
1073.025 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLSPASVCRTH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|--------|------------|--------|----|----------------------|-------------------|
| | | Match | Length | | | |
| 1 | 2534 | 78.6 | 483 | 2 | US-09-949-016-10002 | Sequence 10002, A |
| 2 | 1059.5 | 32.9 | 623 | 1 | US-08-332-838-2 | Sequence 2, Appli |
| 3 | 1018.5 | 31.6 | 584 | 2 | US-09-902-540-15870 | Sequence 15870, A |
| 4 | 1006.5 | 31.2 | 650 | 2 | US-10-363-937-5 | Sequence 5, Appli |
| 5 | 1005.5 | 31.2 | 650 | 2 | US-09-443-795-1 | Sequence 1, Appli |
| 6 | 840.5 | 26.1 | 362 | 2 | US-09-270-767-43340 | Sequence 43340, A |
| 7 | 785.5 | 24.4 | 587 | 2 | US-09-949-016-9933 | Sequence 9933, Ap |
| 8 | 783 | 24.3 | 429 | 2 | US-09-248-796A-17980 | Sequence 17980, A |
| 9 | 557.5 | 17.3 | 285 | 2 | US-09-270-767-42260 | Sequence 42260, A |
| 10 | 341 | 10.6 | 972 | 2 | US-08-335-844A-23 | Sequence 23, Appl |
| 11 | 341 | 10.6 | 972 | 2 | US-09-129-366-23 | Sequence 23, Appl |

| | | | | | | |
|----|-------|------|------|---|----------------------|-------------------|
| 12 | 340.5 | 10.6 | 1025 | 1 | US-08-530-792D-23 | Sequence 23, Appl |
| 13 | 337 | 10.4 | 972 | 2 | US-08-335-844A-24 | Sequence 24, Appl |
| 14 | 337 | 10.4 | 972 | 2 | US-09-129-366-24 | Sequence 24, Appl |
| 15 | 330 | 10.2 | 1026 | 1 | US-08-530-792D-22 | Sequence 22, Appl |
| 16 | 328 | 10.2 | 923 | 2 | US-09-328-352-4371 | Sequence 4371, Ap |
| 17 | 324 | 10.0 | 919 | 2 | US-09-919-039-222 | Sequence 222, App |
| 18 | 311 | 9.6 | 354 | 2 | US-09-949-016-6929 | Sequence 6929, Ap |
| 19 | 304.5 | 9.4 | 990 | 2 | US-10-363-937-7 | Sequence 7, Appli |
| 20 | 304 | 9.4 | 977 | 2 | US-08-335-844A-22 | Sequence 22, Appl |
| 21 | 304 | 9.4 | 977 | 2 | US-09-129-366-22 | Sequence 22, Appl |
| 22 | 298.5 | 9.3 | 957 | 2 | US-09-949-016-6154 | Sequence 6154, Ap |
| 23 | 298.5 | 9.3 | 964 | 2 | US-09-949-016-7431 | Sequence 7431, Ap |
| 24 | 298.5 | 9.3 | 967 | 2 | US-09-139-802-201 | Sequence 201, App |
| 25 | 298.5 | 9.3 | 967 | 2 | US-09-659-786-201 | Sequence 201, App |
| 26 | 297 | 9.2 | 850 | 2 | US-09-902-540-10199 | Sequence 10199, A |
| 27 | 297 | 9.2 | 867 | 2 | US-09-540-236-3193 | Sequence 3193, Ap |
| 28 | 296.5 | 9.2 | 699 | 2 | US-09-270-767-45507 | Sequence 45507, A |
| 29 | 291.5 | 9.0 | 848 | 2 | US-09-583-110-2738 | Sequence 2738, Ap |
| 30 | 290.5 | 9.0 | 912 | 2 | US-09-902-540-16181 | Sequence 16181, A |
| 31 | 285 | 8.8 | 948 | 2 | US-09-620-312D-1105 | Sequence 1105, Ap |
| 32 | 284 | 8.8 | 917 | 2 | US-09-902-540-12845 | Sequence 12845, A |
| 33 | 281.5 | 8.7 | 941 | 2 | US-09-991-181-353 | Sequence 353, App |
| 34 | 281.5 | 8.7 | 941 | 2 | US-09-990-444-353 | Sequence 353, App |
| 35 | 281.5 | 8.7 | 941 | 2 | US-09-997-333-353 | Sequence 353, App |
| 36 | 281.5 | 8.7 | 941 | 2 | US-09-992-598-353 | Sequence 353, App |
| 37 | 273 | 8.5 | 874 | 2 | US-09-489-039A-12124 | Sequence 12124, A |
| 38 | 264.5 | 8.2 | 815 | 2 | US-09-107-433-5059 | Sequence 5059, Ap |
| 39 | 259.5 | 8.0 | 458 | 2 | US-09-602-777A-124 | Sequence 124, App |
| 40 | 258 | 8.0 | 896 | 2 | US-09-543-681A-7870 | Sequence 7870, Ap |
| 41 | 245.5 | 7.6 | 867 | 2 | US-09-602-777A-104 | Sequence 104, App |
| 42 | 245 | 7.6 | 990 | 2 | US-09-657-931A-11 | Sequence 11, Appl |
| 43 | 244.5 | 7.6 | 891 | 2 | US-09-252-991A-28689 | Sequence 28689, A |
| 44 | 244.5 | 7.6 | 986 | 2 | US-09-657-931A-12 | Sequence 12, Appl |
| 45 | 242 | 7.5 | 995 | 2 | US-09-657-931A-1 | Sequence 1, Appli |

OM protein - protein search, using sw model

Run on: November 25, 2005, 19:11:02 ; Search time 166 Seconds
(without alignments)
1535.397 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLSPASVCRTH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|---------------------|-------------------|
| 1 | 3225 | 100.0 | 611 | 5 | US-10-873-595-6 | Sequence 6, Appli |
| 2 | 3222 | 99.9 | 611 | 4 | US-10-247-671-128 | Sequence 128, App |
| 3 | 2963 | 91.9 | 625 | 3 | US-09-925-302-449 | Sequence 449, App |
| 4 | 2963 | 91.9 | 625 | 3 | US-09-925-302-449 | Sequence 449, App |
| 5 | 1464 | 45.4 | 587 | 4 | US-10-369-493-5965 | Sequence 5965, Ap |
| 6 | 1376.5 | 42.7 | 809 | 4 | US-10-369-493-6198 | Sequence 6198, Ap |
| 7 | 1338 | 41.5 | 613 | 6 | US-11-097-143-42687 | Sequence 42687, A |
| 8 | 1206.5 | 37.4 | 612 | 4 | US-10-369-493-22710 | Sequence 22710, A |
| 9 | 1134.5 | 35.2 | 671 | 4 | US-10-369-493-1987 | Sequence 1987, Ap |
| 10 | 1079 | 33.5 | 694 | 4 | US-10-369-493-3998 | Sequence 3998, Ap |
| 11 | 1030.5 | 32.0 | 573 | 4 | US-10-369-493-19241 | Sequence 19241, A |

| | | | | | | |
|----|--------|------|------|---|----------------------|-------------------|
| 12 | 1006.5 | 31.2 | 650 | 4 | US-10-363-937-5 | Sequence 5, Appli |
| 13 | 1006.5 | 31.2 | 650 | 4 | US-10-275-107-66 | Sequence 66, Appl |
| 14 | 1006.5 | 31.2 | 650 | 6 | US-11-167-040-5 | Sequence 5, Appli |
| 15 | 1005.5 | 31.2 | 650 | 3 | US-09-854-875A-1 | Sequence 1, Appli |
| 16 | 1005.5 | 31.2 | 650 | 4 | US-10-056-253-1 | Sequence 1, Appli |
| 17 | 1005.5 | 31.2 | 650 | 5 | US-10-767-308-1 | Sequence 1, Appli |
| 18 | 987 | 30.6 | 626 | 4 | US-10-108-260A-4299 | Sequence 4299, Ap |
| 19 | 954 | 29.6 | 569 | 4 | US-10-369-493-9160 | Sequence 9160, Ap |
| 20 | 947 | 29.4 | 671 | 4 | US-10-369-493-17597 | Sequence 17597, A |
| 21 | 929.5 | 28.8 | 588 | 4 | US-10-369-493-15968 | Sequence 15968, A |
| 22 | 929.5 | 28.8 | 588 | 4 | US-10-369-493-16330 | Sequence 16330, A |
| 23 | 929.5 | 28.8 | 641 | 4 | US-10-369-493-15592 | Sequence 15592, A |
| 24 | 892.5 | 27.7 | 611 | 4 | US-10-425-115-272788 | Sequence 272788, |
| 25 | 887.5 | 27.5 | 650 | 4 | US-10-425-114-61058 | Sequence 61058, A |
| 26 | 880.5 | 27.3 | 611 | 4 | US-10-437-963-143613 | Sequence 143613, |
| 27 | 880 | 27.3 | 540 | 4 | US-10-369-493-9417 | Sequence 9417, Ap |
| 28 | 874 | 27.1 | 581 | 4 | US-10-369-493-17802 | Sequence 17802, A |
| 29 | 800.5 | 24.8 | 724 | 4 | US-10-275-107-67 | Sequence 67, Appl |
| 30 | 800 | 24.8 | 725 | 3 | US-09-929-218-2 | Sequence 2, Appli |
| 31 | 800 | 24.8 | 725 | 4 | US-10-423-543-40 | Sequence 40, Appl |
| 32 | 766.5 | 23.8 | 416 | 4 | US-10-296-115-1194 | Sequence 1194, Ap |
| 33 | 593 | 18.4 | 363 | 4 | US-10-767-701-42438 | Sequence 42438, A |
| 34 | 534 | 16.6 | 358 | 4 | US-10-424-599-157271 | Sequence 157271, |
| 35 | 517 | 16.0 | 416 | 4 | US-10-311-035-3 | Sequence 3, Appli |
| 36 | 401 | 12.4 | 393 | 4 | US-10-099-322-301 | Sequence 301, App |
| 37 | 401 | 12.4 | 393 | 4 | US-10-044-564-301 | Sequence 301, App |
| 38 | 365.5 | 11.3 | 821 | 4 | US-10-369-493-19382 | Sequence 19382, A |
| 39 | 362 | 11.2 | 441 | 4 | US-10-007-271-4 | Sequence 4, Appli |
| 40 | 353.5 | 11.0 | 875 | 4 | US-10-369-493-20117 | Sequence 20117, A |
| 41 | 347.5 | 10.8 | 438 | 4 | US-10-281-904-4 | Sequence 4, Appli |
| 42 | 345.5 | 10.7 | 799 | 4 | US-10-425-115-205689 | Sequence 205689, |
| 43 | 344 | 10.7 | 694 | 4 | US-10-087-192-1851 | Sequence 1851, Ap |
| 44 | 343 | 10.6 | 723 | 4 | US-10-369-493-10942 | Sequence 10942, A |
| 45 | 342 | 10.6 | 1025 | 4 | US-10-087-192-1854 | Sequence 1854, Ap |

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:02:46 ; Search time 5 Seconds
(without alignments)
369.778 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLSPASVCRTH.....HKASHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|--------------------|-------------------|
| | | Match | Length | | | |
| 1 | 342 | 10.6 | 1092 | 1 | US-10-821-234-999 | Sequence 999, App |
| 2 | 281.5 | 8.7 | 941 | 1 | US-10-131-826A-464 | Sequence 464, App |
| 3 | 252.5 | 7.8 | 1024 | 1 | US-10-131-826A-198 | Sequence 198, App |
| 4 | 93 | 2.9 | 2323 | 1 | US-10-793-626-760 | Sequence 760, App |
| 5 | 91.5 | 2.8 | 406 | 1 | US-10-131-826A-502 | Sequence 502, App |
| 6 | 87 | 2.7 | 903 | 7 | US-11-057-058-65 | Sequence 65, Appl |
| 7 | 86.5 | 2.7 | 314 | 1 | US-10-793-626-2552 | Sequence 2552, Ap |
| 8 | 85 | 2.6 | 434 | 1 | US-10-821-234-1553 | Sequence 1553, Ap |
| 9 | 85 | 2.6 | 871 | 7 | US-11-077-550-2 | Sequence 2, Appli |

| | | | | | | |
|----|------|-----|------|---|--------------------|-------------------|
| 10 | 85 | 2.6 | 871 | 7 | US-11-077-550-8 | Sequence 8, Appli |
| 11 | 85 | 2.6 | 871 | 7 | US-11-077-550-26 | Sequence 26, Appl |
| 12 | 85 | 2.6 | 871 | 7 | US-11-077-550-153 | Sequence 153, App |
| 13 | 85 | 2.6 | 873 | 7 | US-11-077-550-6 | Sequence 6, Appli |
| 14 | 85 | 2.6 | 873 | 7 | US-11-077-550-149 | Sequence 149, App |
| 15 | 85 | 2.6 | 873 | 7 | US-11-077-550-151 | Sequence 151, App |
| 16 | 85 | 2.6 | 879 | 7 | US-11-077-550-159 | Sequence 159, App |
| 17 | 85 | 2.6 | 894 | 7 | US-11-077-550-4 | Sequence 4, Appli |
| 18 | 85 | 2.6 | 1127 | 7 | US-11-077-550-40 | Sequence 40, Appl |
| 19 | 85 | 2.6 | 1129 | 7 | US-11-077-550-42 | Sequence 42, Appl |
| 20 | 84.5 | 2.6 | 944 | 7 | US-11-057-058-68 | Sequence 68, Appl |
| 21 | 84 | 2.6 | 556 | 1 | US-10-821-234-1509 | Sequence 1509, Ap |
| 22 | 84 | 2.6 | 3056 | 7 | US-11-109-156-20 | Sequence 20, Appl |
| 23 | 83.5 | 2.6 | 1130 | 7 | US-11-077-550-139 | Sequence 139, App |
| 24 | 83 | 2.6 | 966 | 7 | US-11-057-058-67 | Sequence 67, Appl |
| 25 | 82.5 | 2.6 | 775 | 1 | US-10-131-826A-120 | Sequence 120, App |
| 26 | 82.5 | 2.6 | 2080 | 1 | US-10-821-234-1640 | Sequence 1640, Ap |
| 27 | 82 | 2.5 | 873 | 7 | US-11-077-550-167 | Sequence 167, App |
| 28 | 82 | 2.5 | 875 | 7 | US-11-077-550-10 | Sequence 10, Appl |
| 29 | 81.5 | 2.5 | 423 | 7 | US-11-184-156-2 | Sequence 2, Appli |
| 30 | 81 | 2.5 | 877 | 7 | US-11-077-550-157 | Sequence 157, App |
| 31 | 80 | 2.5 | 485 | 1 | US-10-630-203-2 | Sequence 2, Appli |
| 32 | 80 | 2.5 | 485 | 7 | US-11-103-037-1 | Sequence 1, Appli |
| 33 | 80 | 2.5 | 532 | 1 | US-10-821-234-918 | Sequence 918, App |
| 34 | 80 | 2.5 | 1304 | 1 | US-10-821-234-1648 | Sequence 1648, Ap |
| 35 | 79.5 | 2.5 | 138 | 1 | US-10-793-626-1540 | Sequence 1540, Ap |
| 36 | 79.5 | 2.5 | 176 | 1 | US-10-793-626-612 | Sequence 612, App |
| 37 | 79.5 | 2.5 | 878 | 7 | US-11-077-550-12 | Sequence 12, Appl |
| 38 | 79.5 | 2.5 | 887 | 7 | US-11-077-550-161 | Sequence 161, App |
| 39 | 79.5 | 2.5 | 907 | 7 | US-11-077-550-16 | Sequence 16, Appl |
| 40 | 79.5 | 2.5 | 953 | 7 | US-11-077-550-14 | Sequence 14, Appl |
| 41 | 79.5 | 2.5 | 1013 | 7 | US-11-077-550-18 | Sequence 18, Appl |
| 42 | 79.5 | 2.5 | 1432 | 1 | US-10-510-386-218 | Sequence 218, App |
| 43 | 79 | 2.4 | 468 | 7 | US-11-054-385-12 | Sequence 12, Appl |
| 44 | 79 | 2.4 | 871 | 7 | US-11-077-550-155 | Sequence 155, App |
| 45 | 79 | 2.4 | 873 | 7 | US-11-077-550-163 | Sequence 163, App |

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:59:55 ; Search time 42 Seconds
(without alignments)
1397.434 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLSPASVCRTKH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|--------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 3225 | 100.0 | 611 | 1 | S65947 | leukotriene-A4 hyd |
| 2 | 3058 | 94.8 | 611 | 1 | JN0066 | leukotriene-A4 hyd |
| 3 | 3043 | 94.4 | 611 | 1 | JC4237 | leukotriene-A4 hyd |
| 4 | 3042.5 | 94.3 | 610 | 1 | S20444 | leukotriene-A4 hyd |
| 5 | 1464 | 45.4 | 587 | 2 | T32546 | hypothetical prote |
| 6 | 1376.5 | 42.7 | 809 | 2 | T32899 | probable leukotrie |
| 7 | 1206.5 | 37.4 | 612 | 2 | T40936 | probable leukotrie |
| 8 | 1134.5 | 35.2 | 671 | 2 | S61099 | leukotriene-A4 hyd |
| 9 | 947 | 29.4 | 671 | 2 | D82675 | aminopeptidase N X |
| 10 | 668 | 20.7 | 360 | 2 | T51870 | hypothetical prote |
| 11 | 388.5 | 12.0 | 785 | 2 | S73098 | aminopeptidase (EC |
| 12 | 354.5 | 11.0 | 844 | 2 | JC4054 | membrane alanyl am |
| 13 | 344.5 | 10.7 | 844 | 2 | S47274 | membrane alanyl am |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 14 | 341 | 10.6 | 1006 | 2 | A59384 | oxytocinase/insuli |
| 15 | 341 | 10.6 | 1025 | 2 | A59383 | oxytocinase/insuli |
| 16 | 340.5 | 10.6 | 916 | 2 | I55441 | vp165 - rat |
| 17 | 337.5 | 10.5 | 843 | 2 | S38364 | membrane alanyl am |
| 18 | 324.5 | 10.1 | 784 | 2 | B90442 | tricorn proteinase |
| 19 | 317 | 9.8 | 920 | 2 | T10052 | aminopeptidase (EC |
| 20 | 313.5 | 9.7 | 866 | 2 | AI1880 | aminopeptidase [im |
| 21 | 310.5 | 9.6 | 988 | 2 | T24668 | hypothetical prote |
| 22 | 308 | 9.6 | 964 | 2 | G96662 | probable aminopept |
| 23 | 307 | 9.5 | 780 | 2 | T37456 | Tricorn proteinase |
| 24 | 305.5 | 9.5 | 869 | 2 | S76720 | hypothetical prote |
| 25 | 302 | 9.4 | 849 | 2 | JC7959 | lysyl aminopeptida |
| 26 | 301.5 | 9.3 | 884 | 2 | T29637 | hypothetical prote |
| 27 | 300 | 9.3 | 849 | 2 | JU0191 | aminopeptidase Y (|
| 28 | 298.5 | 9.3 | 957 | 2 | A47531 | glutamyl aminopept |
| 29 | 298.5 | 9.3 | 967 | 2 | A30325 | membrane alanyl am |
| 30 | 297 | 9.2 | 472 | 2 | A75464 | probable zinc meta |
| 31 | 296.5 | 9.2 | 990 | 2 | JC8058 | laeverin - human |
| 32 | 291.5 | 9.0 | 848 | 2 | B97960 | membrane alanyl am |
| 33 | 290.5 | 9.0 | 848 | 2 | E95092 | aminopeptidase N [|
| 34 | 289 | 9.0 | 747 | 2 | T23882 | hypothetical prote |
| 35 | 285 | 8.8 | 805 | 2 | S07099 | membrane alanyl am |
| 36 | 284.5 | 8.8 | 882 | 2 | T39789 | aminopeptidase - f |
| 37 | 281 | 8.7 | 862 | 2 | G87094 | probable aminopept |
| 38 | 281 | 8.7 | 963 | 2 | A53984 | membrane alanyl am |
| 39 | 279 | 8.7 | 965 | 2 | A32852 | membrane alanyl am |
| 40 | 277 | 8.6 | 861 | 2 | B70866 | probable aminopept |
| 41 | 275.5 | 8.5 | 844 | 2 | S37794 | aminopeptidase ysc |
| 42 | 274.5 | 8.5 | 945 | 2 | S30398 | aminopeptidase N h |
| 43 | 274 | 8.5 | 786 | 2 | T23883 | hypothetical prote |
| 44 | 274 | 8.5 | 919 | 2 | S42842 | T16G12.2 protein - |
| 45 | 273 | 8.5 | 783 | 2 | T37457 | Tricorn proteinase |

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:59:39 ; Search time 231 Seconds
(without alignments)
1863.083 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLSPASVCRTKH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|--------|-------------|--------|----|--------------|--------------------|--|
| No. | Score | Query Match | Length | DB | ID | Description | |
| 1 | 3225 | 100.0 | 610 | 1 | LKHA4_HUMAN | P09960 homo sapien | |
| 2 | 3225 | 100.0 | 611 | 2 | Q6IAT6_HUMAN | Q6iat6 homo sapien | |
| 3 | 3202 | 99.3 | 611 | 2 | Q5REQ3_PONPY | Q5req3 pongo pygma | |
| 4 | 3090 | 95.8 | 610 | 1 | LKHA4_CHILA | Q6s9c8 chinchilla | |
| 5 | 3061 | 94.9 | 610 | 1 | LKHA4_MOUSE | P24527 mus musculu | |
| 6 | 3043 | 94.4 | 610 | 1 | LKHA4_CAVPO | P19602 cavia porce | |
| 7 | 3042.5 | 94.3 | 609 | 1 | LKHA4_RAT | P30349 rattus norv | |
| 8 | 2540.5 | 78.8 | 612 | 2 | Q5ZJJ6_CHICK | Q5zjj6 gallus gall | |
| 9 | 2294.5 | 71.1 | 609 | 2 | Q6IP81_XENLA | Q6ip81 xenopus lae | |
| 10 | 2284.5 | 70.8 | 609 | 2 | Q6GL78_XENTR | Q6gl78 xenopus tro | |
| 11 | 2190.5 | 67.9 | 611 | 2 | Q5RIF1_BRARE | Q5rif1 brachydanio | |
| 12 | 2180.5 | 67.6 | 611 | 2 | Q6NUX4_BRARE | Q6nux4 brachydanio | |
| 13 | 2077.5 | 64.4 | 630 | 2 | Q4T8V9_TETNG | Q4t8v9 tetraodon n | |
| 14 | 1487 | 46.1 | 625 | 2 | O44183_CAEEL | O44183 caenorhabdi | |
| 15 | 1480 | 45.9 | 625 | 2 | Q61MW9_CAEER | Q61mw9 caenorhabdi | |

| | | | | | | |
|----|--------|------|------|---|--------------|--------------------|
| 16 | 1386.5 | 43.0 | 558 | 2 | Q7Q192_ANOGA | Q7q192 anopheles g |
| 17 | 1376.5 | 42.7 | 609 | 2 | O44969_CAEEL | O44969 caenorhabdi |
| 18 | 1369 | 42.4 | 608 | 2 | Q86GU4_CAEEL | Q86gu4 caenorhabdi |
| 19 | 1338 | 41.5 | 613 | 2 | Q7KT44_DROME | Q7kt44 drosophila |
| 20 | 1338 | 41.5 | 684 | 2 | Q9VJ39_DROME | Q9vj39 drosophila |
| 21 | 1315 | 40.8 | 606 | 2 | Q55BR5_DICDI | Q55br5 dictyosteli |
| 22 | 1212.5 | 37.6 | 614 | 2 | Q4X265_ASPFU | Q4x265 aspergillus |
| 23 | 1206.5 | 37.4 | 612 | 1 | LKHA4_SCHPO | O94544 schizosacch |
| 24 | 1199.5 | 37.2 | 647 | 2 | Q6C3E5_YARLI | Q6c3e5 yarrowia li |
| 25 | 1196.5 | 37.1 | 639 | 2 | Q4HXX0_GIBZE | Q4hxx0 gibberella |
| 26 | 1149.5 | 35.6 | 662 | 2 | Q6CLD3_KLULA | Q6cld3 kluyveromyc |
| 27 | 1145.5 | 35.5 | 652 | 2 | Q6FTM0_CANGA | Q6ftm0 candida gla |
| 28 | 1144.5 | 35.5 | 639 | 2 | Q5B0W8_EMENI | Q5b0w8 aspergillus |
| 29 | 1141 | 35.4 | 614 | 2 | Q7S785_NEUCR | Q7s785 neurospora |
| 30 | 1136 | 35.2 | 1297 | 2 | Q4PI93_USTMA | Q4pi93 ustilago ma |
| 31 | 1134.5 | 35.2 | 671 | 1 | LKHA4_YEAST | Q10740 saccharomyc |
| 32 | 1126 | 34.9 | 613 | 2 | Q51X77_MAGGR | Q51x77 magnaporthe |
| 33 | 1110 | 34.4 | 632 | 2 | Q55RS1_CRYNE | Q55rs1 cryptococcu |
| 34 | 1097.5 | 34.0 | 641 | 2 | Q6BW21_DEBHA | Q6bw21 debaryomyce |
| 35 | 1090 | 33.8 | 626 | 2 | Q6DGD8_BRARE | Q6dgd8 brachydanio |
| 36 | 1084 | 33.6 | 219 | 2 | Q59ES1_HUMAN | Q59es1 homo sapien |
| 37 | 1060.5 | 32.9 | 623 | 2 | Q59NB8_CANAL | Q59nb8 candida alb |
| 38 | 1026.5 | 31.8 | 618 | 2 | Q6NVR0_XENTR | Q6nvr0 xenopus tro |
| 39 | 1018.5 | 31.6 | 618 | 2 | Q6GQ32_XENLA | Q6gq32 xenopus lae |
| 40 | 1016.5 | 31.5 | 612 | 2 | Q641C7_XENLA | Q641c7 xenopus lae |
| 41 | 1014 | 31.4 | 650 | 1 | AMPB_MOUSE | Q8vct3 mus musculu |
| 42 | 1008.5 | 31.3 | 658 | 2 | Q7RU04_HUMAN | Q7ru04 homo sapien |
| 43 | 1006.5 | 31.2 | 650 | 1 | AMPB_HUMAN | Q9h4a4 homo sapien |
| 44 | 1005.5 | 31.2 | 286 | 2 | Q5TZ09_BRARE | Q5tz09 brachydanio |
| 45 | 1001.5 | 31.1 | 650 | 1 | AMPB_RAT | O09175 rattus norv |